REMARKS

This document is filed in reply to the Office Action dated July 26, 2006 ("Office Action"). Applicants have amended claims 1 and 29 to more clearly set forth the claimed invention. Support for the amendments can be found in the specification at, e.g., page 25, Paragraphs 66 and 67, and Figure 1. No new matter has been introduced.

Claims 1-51 are pending. Among them, claims 6-28, 34, and 39-51 have been withdrawn from further consideration for covering a non-elected invention. Claims 1-5, 29-33, and 35-38 will be under examination. Reconsideration of this application is requested in view of the following remarks.

The Examiner rejected claims 1-3, 29-31, 35, and 37 for obviousness over U.S. Patent No. 6,309,840 to Wang *et al.*, ("Wang") in view of U.S. Patent No. 6,599,840 to Honeycutt *et al.* ("Honeycutt"). See the Office Action, page 3, last paragraph. Applicants respectfully traverse.

Claim 1, as amended, covers a method for preparing an array for authenticating whether a plant sample is originated from a known plant. The method comprises the steps of: a) extracting DNA from the known plant; b) amplifying a variable region from the extracted DNA to obtain a nucleotide sequence of the variable region; c) designing specific primers containing one forward primer and a plurality of reverse primers according to the nucleotide sequence; d) amplifying the variable region by separated PCRs with combinations of the specific primers to obtain DNA fragments having different sizes; and e) dotting the DNA fragments onto a solid support.

Wang teaches a method of using PCR-restriction fragment length polymorphism (PCR-RFLP) to authenticate Chinese medicinal herbs. As pointed out by the Examiner, the Wang method is conducted by (a) extracting rDNA from a herb sample with known identity determined by traditional means; (b) amplifying the ITS1-5.8S-ITS2 region of the extracted rDNA using oligonucleotide primers that are conserved across plant kingdom and that flank to the ITS1-5.8S-ITS2 region by polymerase chain reaction; (c) digesting the amplified ITS1-5.8S-ITS2 region with appropriate restriction endonucleases to generate restriction fragments; and (d) separating the restriction fragments resulted from step (c) to generate profiles and comparing these profiles with the known profiles from an authenticated sample with the same identity, wherein similar profiles confirm the identity of the herbal sample. See Wang, column 5, lines 20-32.

The Examiner acknowledged that "Wang does not specifically teach analyzing and comparing the known plants and unknown plants using dotting the DNA fragments on a solid support." See the Office Action, page 4, lines 17-18. However, the Examiner alleged that Honeycutt teaches identifying organisms by detecting differences among taxonomic groupings of organisms using solid supports. See the Office Action, page 4, last paragraph. She then proceeded to conclude that "it would have been prima facie obvious to the ordinary artisan at the time the invention was made to have modified the RFLP detection method of Wang with the array based method of Honeycutt for the expected benefits of high throughput analysis." See the Office Action, page 5, second paragraph.

Applicants note that, as pointed out above, the method of amended claim 1 requires amplifying a variable region by separated PCRs with combinations of the specific primers to obtain DNA fragments having different sizes. See step d). In contrast, Wang and Honeycutt, combined or alone, do not teach or suggest this step. Thus, they do not render claim 1 obvious.

Further, the method of claim 1 requires two amplifying steps: b) and d). Wang and Honeycutt, combined or alone, do not teach or suggest two amplifying steps. Thus, claim 1 is non-obvious on this additional ground.

Claim 29, as amended, is drawn to a method for determining whether a plant sample is originated from a known plant. Like that of amended claim 1, this method also requires (i) step d) amplifying a variable region by separated PCRs with combinations of the specific primers to obtain DNA fragments having different sizes and (ii) two amplifying steps: b) and d). For the same reasons set forth above, the method of amended claim 9 is patentable over Wang and Honeycutt.

In addition, the method of amended claim 29 requires processing hybridization signals to determine whether the plant sample is originated from a known plant based on a linear relationship between the hybridization signal and the fragment size. See step i). None of Wang or Honeycutt teaches or suggests this linear relationship, much less a method utilizing this linear relationship. Thus, amended claim 29 is patentable over the two references on this additional ground.

For the above remarks, Applicants submit that claims 1 and 29 are non-obvious over Wang and Honeycutt. So are claims 2, 3, 30-33, 35, and 37, all of which depend from claim 1 or

29.

The Examiner also rejected claims 4 and 32 for obviousness over Wang in view of Honeycutt and a webpage on the same ground discussed above. See the Office Action, page 6, second paragraph. For the same reasons set forth above, Applicants respectfully submit claims 4 and 32 are patentable over the three references.

CONCLUSION

Applicants submit that ground for the rejection asserted by the Examiner have been overcome, and that claims, as pending, define subject matter that is non-obvious. On this basis, it is submitted that allowance of this application is proper, and early favorable action is solicited.

Please apply any charges to deposit account 06-1050, referencing attorney docket 17329-002001.

Respectfully submitted,

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